**IN THE CLAIMS**

This listing of claims will replace all prior versions, and listings, of the claims in the application.

1. (*Currently amended*) A method of managing and retrieving biological data for efficient exploration and analysis, the method comprising:

acquiring ~~and staging~~ gene expression data for storage, wherein the gene expression data comprises hybridization experiment data from microarray samples prepared from tissues and cell lines;

applying a quality control process to mask defective data points within the gene expression data and to enforce a sample completion constraint;

staging the gene expression data, wherein staging comprises linking the gene expression data with sample data and a fragment index;

storing the linked gene expression data, sample data and fragment index in a data warehouse comprising three distinct databases comprising a gene expression database for storing quantitative gene expression measurements for the tissues and cell lines, a clinical database for storing the sample data comprising information on bio-samples and donors from which the tissues and cell lines were obtained, and a fragment index database for storing information on biological properties and gene sequences for DNA fragments in microarrays from which the gene expression measurements were obtained, wherein the data warehouse is arranged in a relational format~~, and wherein staging comprises linking gene expression measurements in the gene expression database with sample data in the clinical database and information in the fragment index database~~;

providing a user interface for entry of a first query, wherein the first query comprises a first sample set or gene set for which additional information is sought, and wherein the sample set comprises a plurality of samples having one or more selected attributes and the gene set comprises at least one gene having one or more selected properties;

receiving the first query;

correlating gene expression measurements within the gene expression database with the first sample set or gene set of the first query; and

displaying at the user interface the correlated gene expression measurements that are responsive to the first query.

2. (*Original*) The method of claim 1, wherein the data warehouse is constructed in a star relational schema.

3. (*Original*) The method of claim 1, wherein the data warehouse is constructed in a snowflake relational schema.

4. (*Previously presented*) The method of claim 1, further comprising a gene signature analysis that comprises analyzing the correlated gene expression measurements to identify a present set of DNA fragments that are present within the first sample set or gene set, and an absent set of DNA fragments that are absent within the first sample set or gene set.

5. (*Previously presented*) The method of claim 4, further comprising a gene signature differential analysis that comprises:

performing a gene signature analysis for a second sample set or gene set;

comparing the two different gene signature analysis results; and

identifying four sets of DNA gene fragments comprising:

a present/absent gene set including fragments that are present within the first sample set or gene set and absent within the second sample set or gene set;

a present/present gene set including fragments that are present within both the first and second sample set or gene set;

an absent/absent gene set including fragments that are absent within both the first and second sample set or gene set; and

an absent/present gene set including fragments that are absent within the first

sample set or gene set and are present within the second sample set or gene set.

6. (*Previously presented*) The method of claim 1, further comprising a fold change analysis that comprises:

calculating mean expression levels for each gene fragment within the first sample set or gene set;

before or after calculating mean expression levels for the first sample set or gene set, correlating gene expression measurements with a second query comprising a second sample set or gene set;

calculating mean expression levels of each gene fragment within the second sample set or gene set; and

comparing the mean expression levels for the two sample sets or gene sets to quantify a change in expression for differentially expressed genes between pairs of DNA fragments.

7. (*Previously presented*) The method of claim 1, further comprising an E Northern analysis that identifies DNA fragments with regard to a pair of user-selected percentiles over the values for a sample.

8. (*Currently amended*) A computer system comprising:

a data management system for acquiring gene expression data, the data management system comprising a quality control module for detecting and masking defective gene expression data and applying data consistency rules;

a data warehouse that comprises three distinct databases comprising a gene expression database for storing quantitative gene expression measurements obtained from microarray samples prepared from tissues and cell lines, a clinical database for storing sample data on bio-samples and donors from which the tissues and cell lines were obtained, and a fragment index database for storing information on biological properties and gene sequences for DNA fragments on microarrays from which the gene expression measurements were obtained, wherein the data

warehouse is arranged in a relational format;

a staging database for linking gene expression measurements ~~in the gene expression database~~ from the data management system with the sample data ~~in the clinical database~~ and the information ~~in the fragment index database~~ on biological properties and gene sequences for DNA fragments on microarrays, and for loading the linked measurements and data into the data warehouse;

a data explorer for accessing and analyzing data in the data warehouse; and

a user interface in communication with the data explorer for entering a first query, wherein the first query comprises a first sample set or gene set for which additional information is sought, and wherein the sample set comprises a plurality of samples having one or more selected attributes and the gene set comprises at least one gene having one or more selected properties, and for displaying the results of a correlation of the gene expression measurements with the first sample set or gene set.

9. (*Original*) The computer of claim 8, wherein the data warehouse is constructed in a star relational schema.

10. (*Original*) The computer of claim 8, wherein the data warehouse is constructed in a snowflake relational schema.

11. (*Previously presented*) The computer of claim 8, wherein the data explorer performs a gene signature analysis comprising analyzing the correlated gene expression measurements to identify a present set of DNA fragments that are present within the first sample set or gene set, and an absent set of DNA fragments that are absent within the first sample set or gene set.

12. (*Previously presented*) The computer of claim 11 , wherein the data explorer performs a gene signature differential analysis comprising:

performing a gene signature analysis for a second sample set or gene set;

comparing the two different gene signature analysis results; and

identifying four sets of DNA gene fragments comprising:

a present/absent gene set including fragments that are present within the first sample set or gene set and absent within the second sample set or gene set;

a present/present gene set including fragments that are present within both the first and second sample set or gene set;

an absent/absent gene set including fragments that are absent within both the first and second sample set or gene set; and

an absent/present set including fragments that are absent within the first sample set or gene set and are present within the second sample set or gene set.

13. (*Previously presented*) The computer of claim 8, wherein the data explorer performs a fold change analysis, comprising:

calculating mean expression levels for each gene fragment within the first sample set or gene set;

before or after calculating mean expression levels for the first sample set or gene set, correlating gene expression measurements with a second query comprising a second sample set or gene set;

calculating mean expression levels of each gene fragment within the second sample set or gene set; and

comparing the mean expression levels for the two sample sets or gene sets to quantify a change in expression for differentially expressed genes between pairs of DNA fragments.

14. (*Previously presented*) The computer of claim 8, wherein the data explorer performs an E Northern analysis that identifies DNA fragments with regard to a pair of user-selected percentiles over the values for a sample.

15. (*Currently amended*) A computer program product comprising a computer-usable

medium having computer-readable program code embodied thereon relating to a data warehouse comprising gene expression data and related information, the computer program product comprising computer-readable program code for effecting the following steps within a computing system:

applying a quality control process to mask defective data points within the gene expression data and to enforce a sample completion constraint;

arranging the data warehouse into three distinct databases comprising a gene expression database for storing quantitative gene expression measurements taken from microarray samples prepared from tissues and cell lines, a clinical database for storing sample data on bio-samples and donors from which the tissues and cell lines were obtained, and a fragment index database for storing information on biological properties and gene sequences for DNA fragments on microarrays from which the gene expression measurements were obtained, wherein the data warehouse is arranged in a relational format;

providing a staging database for linking gene expression measurements in the gene expression database with sample data in the clinical database and information in the fragment index database, and loading the linked measurements and data into the data warehouse;

providing a user interface for entry of a first query, wherein the first query comprises a first sample set or gene set for which additional information is sought, and wherein the sample set comprises a plurality of samples having one or more selected attributes and the gene set comprises at least one gene having one or more selected properties;

correlating gene expression measurements within the gene expression database with the sample set or gene set of the first query; and

displaying at the user interface the correlated gene expression measurements that are responsive to the first query.

16. (*Original*) The computer program product of claim 15, wherein the data warehouse is constructed in a star relational schema.

17. (*Original*) The computer program product of claim 15, wherein the data warehouse is constructed in a snowflake relational schema.

18. (*Previously presented*) The computer program product of claim 15, further comprising computer-readable program code for effecting a gene signature analysis comprising analyzing the correlated gene expression measurements to identify a present set of DNA fragments that are present within the first sample set or gene set, and an absent set of DNA fragments that are absent within the first sample set or gene set.

19. (*Previously presented*) The computer program product of claim 18, further comprising computer-readable program code for effecting a gene signature differential analysis and the method further comprises:

performing a gene signature analysis for a second sample set or gene set;

comparing the two different gene signature analysis results; and

identifying four sets of DNA gene fragments comprising:

a present/absent gene set including fragments that are present within the first sample set or gene set and absent within the second sample set or gene set;

a present/present gene set including fragments that are present within both the first and second sample set or gene set;

an absent/absent gene set including fragments that are absent within both the first and second sample set or gene set; and

an absent/present gene set including fragments that are absent within the first sample set or gene set and are present within the second sample set or gene set.

20. (*Previously presented*) The computer program product of claim 15, further comprising computer-readable program code for effecting a fold change analysis comprising:

calculating mean expression levels for each gene fragment within the first sample set or gene set;

before or after calculating mean expression levels for the first sample set or gene set, correlating gene expression measurements with a second query comprising a second sample set or gene set;

calculating mean expression levels of each gene fragment within the second sample set or gene set; and

comparing the mean expression levels for the two sample sets or gene sets to quantify a change in expression for differentially expressed genes between pairs of DNA fragments.

21. (*Previously presented*) The method of claim 15, further comprising computer-readable program code for effecting an E Northern analysis that identifies DNA fragments with regard to a pair of user-selected percentiles over the values for a sample.